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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/007,267

DATE: 03/21/2002
TIME: 14:06:43

Input Set : N:\Crif3\RULE60\10007267.raw
Output Set: N:\CRF3\03212002\J007267.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

- 2 (i) APPLICANT: Gotschlich, Emil C.
- 3 (ii) TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
- 4 OLIGOSACCHARIDES, AND GENES ENCODING THEM
- 5 (iii) NUMBER OF SEQUENCES: 12
- 6 (iv) CORRESPONDENCE ADDRESS:
 - 7 (A) ADDRESSEE: Klauber & Jackson
 - 8 (B) STREET: 411 Hackensack Avenue
 - 9 (C) CITY: Hackensack
 - 10 (D) STATE: New Jersey
 - 11 (E) COUNTRY: USA
 - 12 (F) ZIP: 07601

ENTERED

13 (v) COMPUTER READABLE FORM:

- 14 (A) MEDIUM TYPE: Floppy disk
- 15 (B) COMPUTER: IBM PC compatible
- 16 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 17 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

18 (vi) CURRENT APPLICATION DATA:

- C--> 19 (A) APPLICATION NUMBER: US/10/007,267
- C--> 20 (B) FILING DATE: 03-Dec-2001
- 21 (C) CLASSIFICATION:

22 (vii) PRIOR APPLICATION DATA:

- 23 (A) APPLICATION NUMBER: US/09/333,412
- 24 (B) FILING DATE: 15-Jun-1999
- 26 (A) APPLICATION NUMBER: 08/312,387
- 27 (B) FILING DATE: July 7, 1994

28 (viii) ATTORNEY/AGENT INFORMATION:

- 29 (A) NAME: Jackson Esq., David A.
- 30 (B) REGISTRATION NUMBER: 26,742
- 31 (C) REFERENCE/DOCKET NUMBER: 600-1-095

32 (ix) TELECOMMUNICATION INFORMATION:

- 33 (A) TELEPHONE: 201 487-5800
- 34 (B) TELEFAX: 201 343-1684
- 35 (C) TELEX: 133521

36 (2) INFORMATION FOR SEQ ID NO: 1:

37 (i) SEQUENCE CHARACTERISTICS:

- 38 (A) LENGTH: 5859 base pairs
- 39 (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: both
- 41 (D) TOPOLOGY: unknown

42 (ii) MOLECULE TYPE: DNA (genomic)

43 (iii) HYPOTHETICAL: NO

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44 (iv) ANTI-SENSE: NO
45 (vi) ORIGINAL SOURCE:
46 (A) ORGANISM: Neisseria gonorrhoeae
47 (B) STRAIN: F62
48 (ix) FEATURE:
49 (A) NAME/KEY: CDS
50 (B) LOCATION: 1..381
51 (C) GENE: glys (glycyl tRNA synthetase beta chain)
52 (ix) FEATURE:
53 (A) NAME/KEY: CDS
54 (B) LOCATION: 445..1491
55 (C) GENE: lgtA
56 (ix) FEATURE:
57 (A) NAME/KEY: CDS
58 (B) LOCATION: 2342..3262
59 (C) GENE: lgtC
60 (ix) FEATURE:
61 (A) NAME/KEY: CDS
62 (B) LOCATION: 3322..4335
63 (C) GENE: lgtD
64 (ix) FEATURE:
65 (A) NAME/KEY: CDS
66 (B) LOCATION: 4354..5196
67 (C) GENE: lgtE
68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
69 CTG CAG GCC GTC GCC GTA TTC AAA CAA CTG CCC GAA GCC GCC GCG CTC 48
70 Leu Gln Ala Val Ala Val Phe Lys Gln Leu Pro Glu Ala Ala Ala Leu
71 1 5 10 15
72 GCC GCC GCC AAC AAA CGC GTG CAA AAC CTG CTG AAA AAA GCC GAT GCC 96
73 Ala Ala Ala Asn Lys Arg Val Gln Asn Leu Leu Lys Lys Ala Asp Ala
74 20 25 30
75 GCG TTG GGC GAA GTC AAT GAA AGC CTG CTG CAA CAG GAC GAA GAA AAA 144
76 Ala Leu Gly Glu Val Asn Glu Ser Leu Leu Gln Gln Asp Glu Glu Lys
77 35 40 45
78 GCC CTG TAC GCT GCC GCG CAA GGT TTG CAG CCG AAA ATT GCC GCC GCC 192
79 Ala Leu Tyr Ala Ala Ala Gln Gly Leu Gln Pro Lys Ile Ala Ala Ala
80 50 55 60
81 GTC GCC GAA GGC AAT TTC CGA ACC GCC TTG TCC GAA CTG GCT TCC GTC 240
82 Val Ala Glu Gly Asn Phe Arg Thr Ala Leu Ser Glu Leu Ala Ser Val
83 65 70 75 80
84 AAG CCG CAG GTT GAT GCC TTC TTC GAC GGC GTG ATG GTG ATG GCG GAA 288
85 Lys Pro Gln Val Asp Ala Phe Phe Asp Gly Val Met Val Met Ala Glu
86 85 90 95
87 GAT GCC GCC GTA AAA CAA AAC CGC CTG AAC CTG CTG AAC CGC TTG GCA 336
88 Asp Ala Ala Val Lys Gln Asn Arg Leu Asn Leu Leu Asn Arg Leu Ala
89 100 105 110
90 GAG CAG ATG AAC GCG GTG GCC GAC ATC GCG CTT TTG GGC GAG TAACCGTTGT 388
91 Glu Gln Met Asn Ala Val Ala Asp Ile Ala Leu Leu Gly Glu
92 115 120 125

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93	ACAGTCCAAA TGCCGTCTGA AGCCTTCAGG CGGCATCAAA TTATCGGGAG AGTAAA	444
94	TTG CAG CCT TTA GTC AGC GTA TTG ATT TGC GCC TAC AAC GTA GAA AAA	492
95	Met Gln Pro Leu Val Ser Val Leu Ile Cys Ala Tyr Asn Val Glu Lys	
W--> 96	1 5 10 15	
97	TAT TTT GCC CAA TCA TTA GCC GCC GTC GTG AAT CAG ACT TGG CGC AAC	540
98	Tyr Phe Ala Gln Ser Leu Ala Ala Val Val Asn Gln Thr Trp Arg Asn	
W--> 99	20 25 30	
100	TTG GAT ATT TTG ATT GTC GAT GAC GGC TCG ACA GAC GGC ACA CTT GCC	588
101	Leu Asp Ile Leu Ile Val Asp Asp Gly Ser Thr Asp Gly Thr Leu Ala	
W--> 102	35 40 45	
103	ATT GCC AAG GAT TTT CAA AAG CGG GAC AGC CGT ATC AAA ATC CTT GCA	636
104	Ile Ala Lys Asp Phe Gln Lys Arg Asp Ser Arg Ile Lys Ile Leu Ala	
W--> 105	50 55 60	
106	CAA GCT CAA AAT TCC GGC CTG ATT CCC TCT TTA AAC ATC GGG CTG GAC	684
107	Gln Ala Gln Asn Ser Gly Leu Ile Pro Ser Leu Asn Ile Gly Leu Asp	
W--> 108	65 70 75 80	
109	GAA TTG GCA AAG TCG GGG GGG GGG GGG GAA TAT ATT GCG CGC ACC	732
110	Glu Leu Ala Lys Ser Gly Gly Gly Gly Glu Tyr Ile Ala Arg Thr	
W--> 111	85 90 95	
112	GAT GCC GAC GAT ATT GCC TCC CCC GGC TGG ATT GAG AAA ATC GTG GGC	780
113	Asp Ala Asp Asp Ile Ala Ser Pro Gly Trp Ile Glu Lys Ile Val Gly	
W--> 114	100 105 110	
115	GAG ATG GAA AAA GAC CGC AGC ATC ATT GCG ATG GGC GCG TGG CTG GAA	828
116	Glu Met Glu Lys Asp Arg Ser Ile Ile Ala Met Gly Ala Trp Leu Glu	
W--> 117	115 120 125	
118	GTT TTG TCG GAA GAA AAG GAC GGC AAC CGG CTG GCG CGG CAC CAC AAA	876
119	Val Leu Ser Glu Glu Lys Asp Gly Asn Arg Leu Ala Arg His His Lys	
W--> 120	130 135 140	
121	CAC GGC AAA ATT TGG AAA AAG CCG ACC CGG CAC GAA GAC ATC GCC GCC	924
122	His Gly Lys Ile Trp Lys Lys Pro Thr Arg His Glu Asp Ile Ala Ala	
W--> 123	145 150 155 160	
124	TTT TTC CCT TTC GGC AAC CCC ATA CAC AAC AAC ACG ATG ATT ATG CGG	972
125	Phe Phe Pro Phe Gly Asn Pro Ile His Asn Asn Thr Met Ile Met Arg	
W--> 126	165 170 175	
127	CGC AGC GTC ATT GAC GGC GGT TTG CGT TAC GAC ACC GAG CGG GAT TGG	1020
128	Arg Ser Val Ile Asp Gly Gly Leu Arg Tyr Asp Thr Glu Arg Asp Trp	
W--> 129	180 185 190	
130	GCG GAA GAT TAC CAA TTT TGG TAC GAT GTC AGC AAA TTG GGC AGG CTG	1068
131	Ala Glu Asp Tyr Gln Phe Trp Tyr Asp Val Ser Lys Leu Gly Arg Leu	
W--> 132	195 200 205	
133	GCT TAT TAT CCC GAA GCC TTG GTC AAA TAC CGC CTT CAC GCC AAT CAG	1116
134	Ala Tyr Tyr Pro Glu Ala Leu Val Lys Tyr Arg Leu His Ala Asn Gln	
W--> 135	210 215 220	
136	GTT TCA TCC AAA CAC AGC GTC CGC CAA CAC GAA ATC GCG CAA GGC ATC	1164
137	Val Ser Ser Lys His Ser Val Arg Gln His Glu Ile Ala Gln Gly Ile	
W--> 138	225 230 235 240	
139	CAA AAA ACC GCC AGA AAC GAT TTT TTG CAG TCT ATG GGT TTT AAA ACC	1212
140	Gln Lys Thr Ala Arg Asn Asp Phe Leu Gln Ser Met Gly Phe Lys Thr	
W--> 141	245 250 255	

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142	CGG TTC GAC AGC CTA GAA TAC CGC CAA ACA AAA GCA GCG GCG TAT GAA	1260
143	Arg Phe Asp Ser Leu Glu Tyr Arg Gln Thr Lys Ala Ala Ala Tyr Glu	
W--> 144	260 265 270	
145	CTG CCG GAG AAG GAT TTG CCG GAA GAA GAT TTT GAA CGC GCC CGC CGG	1308
146	Leu Pro Glu Lys Asp Leu Pro Glu Glu Asp Phe Glu Arg Ala Arg Arg	
W--> 147	275 280 285	
148	TTT TTG TAC CAA TGC TTC AAA CGG ACG GAC ACG CCG CCC TCC GGC GCG	1356
149	Phe Leu Tyr Gln Cys Phe Lys Arg Thr Asp Thr Pro Pro Ser Gly Ala	
W--> 150	290 295 300	
151	TGG CTG GAT TTC GCG GCA GAC GGC AGG ATG AGG CGG CTG TTT ACC TTG	1404
152	Trp Leu Asp Phe Ala Ala Asp Gly Arg Met Arg Arg Leu Phe Thr Leu	
W--> 153	305 310 315 320	
154	AGG CAA TAC TTC GGC ATT TTG TAC CGG CTG ATT AAA AAC CGC CGG CAG	1452
155	Arg Gln Tyr Phe Gly Ile Leu Tyr Arg Leu Ile Lys Asn Arg Arg Gln	
W--> 156	325 330 335	
157	GCG CGG TCG GAT TCG GCA GGG AAA GAA CAG GAG ATT TAATGCAAAA	1498
158	Ala Arg Ser Asp Ser Ala Gly Lys Glu Gln Glu Ile	
W--> 159	340 345	
160	CCACGTTATC AGCTTGGCTT CCGCCGCAGA ACGCAGGGCG CACATTGCCG CAACCTTCGG	1558
161	CAGTCGCGGC ATCCCGTTCC AGTTTTTCGA CGCACTGATG CCGTCTGAAA GGCTGGAACG	1618
162	GGCAATGGCG GAACTCGTCC CCGGCTTGTC GGCGCACCCC TATTTGAGCG GAGTGGAAAA	1678
163	AGCCTGCTTT ATGAGCCACG CCGTATTGTG GGAACAGGCA TTGGACGAAG GCGTACCGTA	1738
164	TATCGCCGTA TTTGAAGATG ATGTCTTACT CGGCGAAGGC GCGGAGCAGT TCCTTGCCGA	1798
165	AGATACTTGG CTGCAAGAAC GCTTTGACCC CGATTCCGCC TTTGTCTGCC GCTTGGA AAC	1858
166	GATGTTTATG CACGTCCTGA CCTCGCCCTC CGGCGTGGCG GACTACGGCG GGCGCGCCTT	1918
167	TCCGCTTTTG GAAAGCGAAC ACTGCGGGAC GGCGGGCTAT ATTATTTCCC GAAAGGCGAT	1978
168	GCGTTTTTTC TTGGACAGGT TTGCCGTTTT GCCGCCCGAA CGCCTGCACC CTGTCTGATTT	2038
169	GATGATGTTT GGCAACCCCTG ACGACAGGGA AGGAATGCCG GTTTGCCAGC TCAATCCCGC	2098
170	CTTGTGCGCC CAAGAGCTGC ATTATGCCAA GTTTCACGAC CAAAACAGCG CATTGGGCAG	2158
171	CCTGATCGAA CATGACCGCC GCCTGAACCG CAAACAGCAA TGGCGCGATT CCCC GCCAA	2218
172	CACATTCAAA CACCGCCTGA TCCGCGCCTT GACCAAAATC GGCAGGGA AAAAGAGAA	2278
173	CCGGCAAAGG CGCGAACAGT TAATCGGCAA GATTATTGTG CCTTTCCAAT AAAAGAGAA	2338
174	AAG ATG GAC ATC GTA TTT GCG GCA GAC GAC AAC TAT GCC GCC TAC CTT	2386
175	Met Asp Ile Val Phe Ala Ala Asp Asp Asn Tyr Ala Ala Tyr Leu	
W--> 176	1 5 10 15	
177	TGC GTT GCG GCA AAA AGC GTG GAA GCG GCC CAT CCC GAT ACG GAA ATC	2434
178	Cys Val Ala Ala Lys Ser Val Glu Ala Ala His Pro Asp Thr Glu Ile	
W--> 179	20 25 30	
180	AGG TTC CAC GTC CTC GAT GCC GGC ATC AGT GAG GAA AAC CGG GCG GCG	2482
181	Arg Phe His Val Leu Asp Ala Gly Ile Ser Glu Glu Asn Arg Ala Ala	
W--> 182	35 40 45	
183	GTT GCC GCC AAT TTG CGG GGG GGG GGT AAT ATC CGC TTT ATA GAC GTA	2530
184	Val Ala Ala Asn Leu Arg Gly Gly Gly Asn Ile Arg Phe Ile Asp Val	
W--> 185	50 55 60	
186	AAC CCC GAA GAT TTC GCC GGC TTC CCC TTA AAC ATC AGG CAC ATT TCC	2578
187	Asn Pro Glu Asp Phe Ala Gly Phe Pro Leu Asn Ile Arg His Ile Ser	
W--> 188	65 70 75	
189	ATT ACG ACT TAT GCC CGC CTG AAA TTG GGC GAA TAC ATT GCC GAT TGC	2626
190	Ile Thr Thr Tyr Ala Arg Leu Lys Leu Gly Glu Tyr Ile Ala Asp Cys	

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W--> 191	80	85	90	95	
192	GAC AAA GTC CTG TAT CTG GAT ACG GAC GTA TTG GTC AGG GAC GGC CTG				2674
193	Asp Lys Val Leu Tyr Leu Asp Thr Asp Val Leu Val Arg Asp Gly Leu				
W--> 194		100	105	110	
195	AAG CCC TTA TGG GAT ACC GAT TTG GGC GGT AAC TGG GTC GGC GCG TGC				2722
196	Lys Pro Leu Trp Asp Thr Asp Leu Gly Gly Asn Trp Val Gly Ala Cys				
W--> 197		115	120	125	
198	ATC GAT TTG TTT GTC GAA AGG CAG GAA GGA TAC AAA CAA AAA ATC GGT				2770
199	Ile Asp Leu Phe Val Glu Arg Gln Glu Gly Tyr Lys Gln Lys Ile Gly				
W--> 200		130	135	140	
201	ATG GCG GAC GGA GAA TAT TAT TTC AAT GCC GGC GTA TTG CTG ATC AAC				2818
202	Met Ala Asp Gly Glu Tyr Tyr Phe Asn Ala Gly Val Leu Leu Ile Asn				
W--> 203		145	150	155	
204	CTG AAA AAG TGG CGG CGG CAC GAT ATT TTC AAA ATG TCC TGC GAA TGG				2866
205	Leu Lys Lys Trp Arg Arg His Asp Ile Phe Lys Met Ser Cys Glu Trp				
W--> 206		160	165	170	175
207	GTG GAA CAA TAC AAG GAC GTG ATG CAA TAT CAG GAT CAG GAC ATT TTG				2914
208	Val Glu Gln Tyr Lys Asp Val Met Gln Tyr Gln Asp Gln Asp Ile Leu				
W--> 209		180	185	190	
210	AAC GGG CTG TTT AAA GGC GGG GTG TGT TAT GCG AAC AGC CGT TTC AAC				2962
211	Asn Gly Leu Phe Lys Gly Gly Val Cys Tyr Ala Asn Ser Arg Phe Asn				
W--> 212		195	200	205	
213	TTT ATG CCG ACC AAT TAT GCC TTT ATG GCG AAC GGG TTT GCG TCC CGC				3010
214	Phe Met Pro Thr Asn Tyr Ala Phe Met Ala Asn Gly Phe Ala Ser Arg				
W--> 215		210	215	220	
216	CAT ACC GAC CCG CTT TAC CTC GAC CGT ACC AAT ACG GCG ATG CCC GTC				3058
217	His Thr Asp Pro Leu Tyr Leu Asp Arg Thr Asn Thr Ala Met Pro Val				
W--> 218		225	230	235	
219	GCC GTC AGC CAT TAT TGC GGC TCG GCA AAG CCG TGG CAC AGG GAC TGC				3106
220	Ala Val Ser His Tyr Cys Gly Ser Ala Lys Pro Trp His Arg Asp Cys				
W--> 221		240	245	250	255
222	ACC GTT TGG GGT GCG GAA CGT TTC ACA GAG TTG GCC GGC AGC CTG ACG				3154
223	Thr Val Trp Gly Ala Glu Arg Phe Thr Glu Leu Ala Gly Ser Leu Thr				
W--> 224		260	265	270	
225	ACC GTT CCC GAA GAA TGG CGC GGC AAA CTT GCC GTC CCG CCG ACA AAG				3202
226	Thr Val Pro Glu Glu Trp Arg Gly Lys Leu Ala Val Pro Pro Thr Lys				
W--> 227		275	280	285	
228	TGT ATG CTT CAA AGA TGG CGC AAA AAG CTG TCT GCC AGA TTC TTA CGC				3250
229	Cys Met Leu Gln Arg Trp Arg Lys Lys Leu Ser Ala Arg Phe Leu Arg				
W--> 230		290	295	300	
231	AAG ATT TAT TGACGGGGCA GGCCGTCTGA AGCCTTCAGA CGGCATCGGA				3299
232	Lys Ile Tyr				
W--> 233		305			
234	CGTATCGGAA AGGAGAAACG GA TTG CAG CCT TTA GTC AGC GTA TTG ATT TGC				3351
235	Met Gln Pro Leu Val Ser Val Leu Ile Cys				
W--> 236		1	5	10	
237	GCC TAC AAC GCA GAA AAA TAT TTT GCC CAA TCA TTG GCC GCC GTA GTG				3399
238	Ala Tyr Asn Ala Glu Lys Tyr Phe Ala Gln Ser Leu Ala Ala Val Val				
W--> 239		15	20	25	

VERIFICATION SUMMARY

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Input Set : N:\Cr3\RULE60\10007267.raw

Output Set: N:\CRF3\03212002\J007267.raw

L:19 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:20 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:102 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:117 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:120 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:126 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:129 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:132 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:141 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:144 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:147 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:153 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:156 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:159 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:176 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:182 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:185 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:188 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:194 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:197 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:200 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:203 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:206 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:209 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:212 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:215 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:218 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:224 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:227 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:230 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:233 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:236 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:239 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:242 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:245 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

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L:248 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:251 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:254 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:257 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1